REMARKS UNDER 37 CFR § 1.111

Formal Matters

Claims 1-56 and 80-100 are pending after entry of the amendments set forth herein.

Claims 1-56 and 80-100 were examined. Claims 1-56 and 80-100 were rejected.

Applicants respectfully request reconsideration of the application in view of the amendments and remarks made herein.

No new matter has been added.

The Office Action

Claims Rejected Under 35 U.S.C. Section 112, First Paragraph

In the Official Action of October 3, 2007, claims 1-56 were rejected under 35 U.S.C. Section 112, first paragraph as failing to comply with the written description requirement. The Examiner asserted that the phrase "that has not been mapped to a chromosome map" does not have support in the original disclosure. Applicants respectfully traverse, since all of the examples of arbitrary gene- and protein-related data described in the specification are data, such as experimental data, that have not yet been mapped to a chromosome map. However, in order to advance the prosecution of the instant application, the phrase rejected by the Examiner has been deleted, without prejudice, above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-56 under 35 U.S.C. Section 112, first paragraph as failing to comply with the written description requirement, as being moot.

Claims Rejected Under 35 U.S.C. Section 112, Second Paragraph

Claims 34-56 and 80-100 were rejected under 35 U.S.C. Section 112, second paragraph as being indefinite. The Examiner asserted that the phrase "tissue exhibiting a known abnormality" is indefinite, since it is unclear to whom, when, and where the abnormality is known. Applicants respectfully submit that it is clear that this phrase refers to abnormalities known to the scientific community, i.e., those of

ordinary skill in the art in the present field. However, in order to advance the prosecution of the present application, the claims have been amended above to delete "known".

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 34-56 and 80-100 under 35 U.S.C. Section 112, second paragraph as being indefinite, as being no longer appropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al.)

Claims 1-3, 7, 12-15 and 27-28 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378). The Examiner asserted that Ben-Dor et al. imports RH data from the Whitehead institute as an external source, and uses identifiers in Table 4 to match them, as described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372.

Applicants respectfully traverse. The markers of Table 4 are not arbitrary gene- or protein-related data, but are the identifiers that are used to locate positions on the chromosome, see page 365, column 1, last paragraph to page 365, column 2, second paragraph, and page 368, column 1, last paragraph to page 368, column 2, first paragraph. Thus, it is respectfully submitted that Ben-Dor et al. dos not import arbitrary gene- or protein-related data, but imports markers which are indicators of chromosome locations to be mapped.

It is further respectfully submitted that Ben-Dor et al. does not read identifiers associated with the gene- or protein-related data, and then match the identifiers with pre-defined identifiers on a chromosome map. To the contrary, the markers imported by Ben-For et al. are identifiers that are indicators of locations on a chromosome map.

The Examiner asserted that a matching process is described at page 372, col. 2, lines 7-23 to page 372, col. 1, lines 1-5 of Ben-Dor et al. Applicants respectfully traverse. This portion of Ben-Dor et al. states that different maps of the same chromosome thus give rise to different estimates of its total physical length. Thus an alogiri8ht is used to find shorter maps which are generally seen as being the more desirable ones. The description further refers to comparing the map created by Ben-Dor et al. with that of the Whitehead Institute. However, the description nowhere discloses or suggests matching identifiers associated with gene- or protein related data, with predefined identifiers on a chromosome map to display the gene- or protein- related data in the proper locations on the chromosome map. To further clarify this distinction, Applicants have amended claim 1 above to further recite that the arbitrary

gene- or protein-related data are displayed adjacent positions on the chromosome map according to said matching the identifiers with the predefined identifiers, It is respectfully submitted that Ben-Dor et al. clearly fails to disclose or suggest this feature.

It is further respectfully submitted that the marker of Whitehead Institute are not displayed adjacent predefined indicators on Ben-Dor et al.'s map. Fig. 6 clearly shows that intersecting lines must be drawn to connect the markers between the different arrangements, since they are not placed adjacent one another.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-3, 7, 12-15 and 27-28 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378), as being clearly inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Stanyon et al.)

Claims 16, 18, 20-26, 29-33 and 55-56 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155). The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claim 1. Further, the rat chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon teach or suggest displaying an expression matrix adjacent a chromosome map.

It is respectfully submitted that there would have been no motivation to combine the references as suggested by the Examiner. However, even if the references were so combined, they would still fail to meet all of the recitations of the present claims since Stanyon et al. fails to make up for the deficiencies of Ben-Dor et al. in meeting all of the recitations of claim 1.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 16, 18, 20-26, 29-33 and 55-56 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al.)

Claims 4-6 and 8-11 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al. (U.S. Patent No. 6,519,583). The Examiner admitted that Ben-Dor et al. does not disclose the use of a display to analyze the data (i.e. zooming in to display the additional data as claimed in the instant set of claims), but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of Koleszar et al. because Koleszar et al. has the advantage of displaying the genomic data of Ben-Dor et al. in a more convenient and user-friendly format.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data having identifiers, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et

al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al. map, as lines are drawn between the two maps to show the differences in locations.

It is further respectfully submitted that Koleszar et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Koleszar et al. teaches methods of graphically displaying computer-based biomolecular sequence information, which may be composed of nucleotide or amino acid sequence information, or both. Thus, Koleszar et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Koleszar et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 4-6 and 8-11 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al. (U.S. Patent No. 6,519,583), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Stanyon et al. and Singer et al.)

Claims 17 and 19 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. as applied to claims 16, 18, 20-26, 29-33 and 55-56 above, and further in view of Singer et al. (U.S. Patent No. 5,866,331). The Examiner admitted that Ben-Dor et al. does not disclose the use of heat maps on a plurality of matrices, but asserted that it would have been obvious to modify the radiation hybrid

ordering method of Ben-Dor et al. in view of Singer et al. by the use of heat maps because Singer et al. uses advanced mapping techniques to better detect hybridization to short sequences.

Applicants respectfully traverse. As noted above, it is respectfully submitted that neither Ben-Dor et al. nor Stanyon et al., whether taken alone or in any proper combination, imports arbitrary gene- or protein- related data having identifiers, reads the identifiers, matches the identifiers with predefined identifiers on at least one of the chromosome maps and displays the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract, and Stanyon et al. is directed to methods of painting probes to mouse and rat chromosomes, imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

It is further respectfully submitted that Singer et al. also fails to teach or suggest importing arbitrary gene- or protein- related data having identifiers, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps. Rather, Singer et al. merely teaches methods for accurately determining the total emission intensity of a single fluorochrome, under imaging conditions. Thus, Singer et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Singer et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination

would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 17 and 19 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Stanyon et al. as applied to claims 16, 18, 20-26, 29-33 and 55-56 above, and further in view of Singer et al. (U.S. Patent No. 5,866,331), as being inappropriate.

Claims 80-100

In view of the above amendment of claim 80 to overcome the rejection under 35 U.S.C. Section 112, second paragraph, it is respectfully submitted that these claims are allowable, as no ground of rejection over art has been made. Accordingly the Examiner is respectfully requested to indicate the allowance of claims 80-100 in the next Official Action.

Conclusion

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10020503-2.

Respectfully submitted,

Date: 1/3/08

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